PATENT
Attorney Docket No. 215099

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:

Tanaka et al.

Application No. 10/038,918

Filed: January 3, 2002

For: NOVEL PROTEOME ANALYSIS METHOD AND DEVICES THEREFOR

Art Unit: 1645

Examiner: Unassigned

AMENDMENTS TO SPECIFICATION AND CLAIMS MADE VIA PRELIMINARY AMENDMENT

(Deletions are indicated by {brackets}, while additions are indicated by underlined text)

IN THE SPECIFICATION:

Paragraph beginning at page 5, line 24:

Thirdly, effective idea, method or a technique for grouping the total proteins contained in a biological sample has not been provided. The number of total proteins expressed from human genes totaling to about 30,000 in number reaches a large number exceeding 100,000. They are subject to splicing after transcription from the same gene, thereby producing proteins having shorter peptide {chain} chains than others {~~in~~}, and to various modifications by sugar, lipid, phosphate group and the like, after translation. As a result, proteins, the target of proteomics, consist of far more complicated molecule groups than the DNA polymer molecule, the target of genomics. Based on these facts, a hypothesis is set up that the only methodology (sequence determination for nucleic acid) based on the only purpose (to determine the nucleic acid sequence) can not elucidate diverse structures and functions of proteome. It is thus very important to group the proteins contained in a biological sample based on some idea before proteome analysis and some attempts at pretreatment has been made up to this day. For example, Moily et al. [Eur. J. Biochem. 267, 2871-2881 (2000)] and Santoni et al. [Electrophoresis 21, 1054-1070 (2000)] pretreated a sample with strong solubilizer, but have not solubilized all proteins. Herbert et al.